

SEQUENCE LISTING

<110> Rhône-Poulenc Rorer
 <120> Polypeptides capable of interacting with
 5 oncogenic mutants of the p53 protein
 <130> Sequences
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 10 <141>
 <150> FR9812754
 <151> 1998-10-12
 15 <160> 33
 <170> PatentIn Ver. 2.1
 <210> 1
 20 <211> 23
 <212> DNA
 <213> Artificial sequence
 <220>
 25 <223> Artificial sequence description: oligonucleotide
 <400> 1
 agatctgtat ggaggagccg cag 23
 <210> 2
 30 <211> 29
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<223> Artificial sequence description: 3'-393
oligonucleotide (p53)

<400> 2
agatctcatc agtctgagtc aggcccttc

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<223> Artificial sequence description: 3' H175
oligonucleotide

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ggggcagtgc ctcac

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<210> 4
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<223> Artificial sequence description: 3' W248
oligonucleotide

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<400> 4
gggcctccag ttcac

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<210> 5
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<223> Artificial sequence description: 3' H273
oligonucleotide

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<210> 6
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<210> 7
<211> 23
<212> DNA
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<223> Artificial sequence description: 5'-73
oligonucleotide

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<400> 7
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<210> 8
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<213> Artificial sequence

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<221> CDS

$\langle 220 \rangle$

<223> Artificial sequence description: murine MBP1

5 C-term fragment

<400> 8
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 Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp
 1 5 10 15
 ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac ctg 96
 Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu
 20 25 30
 ccg ggc tcc ttc cga tgc cag tgt gag cca ggc ttc cag ttg gga cct 144
 Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
 35 40 45
 aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc cca 192
 Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
 50 55 60
 tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgt 240
 Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys
 65 70 75 80
 aac cag ggc tat gag ctg cac cgg gat ggc ttc tcc tgc agc gat atc 288
 Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile
 85 90 95
 gat gag tgc ggc tac tcc agt tac ctc tgc cag tac cgc tgt gtc aac 336
 Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn
 100 105 110
 gag cca ggc cga ttc tcc tgt cac tgc cca caa ggc tac cag ctg ctg 384
 Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu
 115 120 125
 gct aca agg ctc tgc caa gat att gac gag tgt gaa aca ggt gca cac 432
 Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His
 130 135 140
 caa tgt tct gag gcc caa acc tgt gtc aac ttc cat ggg ggt tac cgc 480
 Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg
 145 150 155 160
 tgt gtg gac acc aac cgt tgt gtg gag ccc tat gtc caa gtg tca gac 528
 Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp
 165 170 175
 aac cgc tgc ctc tgc cct gcc tcc aat ccc ctt tgt cga gag cag cct 576
 Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro
 180 185 190
 tca tcc att gtg cac cgc tac atg agc atc acc tca gag cga agt gtg 624
 Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val
 195 200 205
 cct gct gac gtg ttc cag atc cag gca acc tct gtc tac cct ggt gcc 672

Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala
 210 215 220
 tac aat gcc ttt cag atc cgt tct gga aac aca cag ggg gac ttc tac 720
 Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr
 225 230 235 240
 att agg caa atc aac aat gtc agc gcc atg ctg gtc ctc gcc agg cca 768
 Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro
 245 250 255
 gtg acg gga ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc atg 816
 Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met
 260 265 270
 aat tcc ctt atg agc tac cgg gcc agc tct gta ctg aga ctc acg gtc 864
 Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val
 275 280 285
 ttt gtg gga gcc tat acc ttc tgaagacct cagggaaggg ccattgtgggg 915
 Phe Val Gly Ala Tyr Thr Phe
 290 295
 gccccctccc cctcccatag cttaagcagc cccggggggcc tagggatgac cgttctgctt 975
 aaaggaacta tgatgtgaag gacaataaag ggagaaagaa ggaaaa. 1021

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 <211> 295
 5 <212> PRT
 <213> Artificial sequence
 <223> Artificial sequence description: murine MBP1
 C-term fragment

<400> 9.

Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp
 1 5 10 15
 Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu
 20 25 30
 Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
 35 40 45
 Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
 50 55 60
 Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys
 65 70 75 80
 Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile
 85 90 95
 Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn
 100 105 110
 Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu
 115 120 125
 Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His
 130 135 140
 Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg
 145 150 155 160
 Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp
 165 170 175
 Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro
 180 185 190
 Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val
 195 200 205
 Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala
 210 215 220
 Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr
 225 230 235 240
 Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro
 245 250 255
 Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met
 260 265 270
 Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val
 275 280 285
 Phe Val Gly Ala Tyr Thr Phe
 290 295

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<210> 10
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 <212> DNA
 <213> Artificial sequence

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<220>
 <223> Artificial sequence description: 5' c-myc
 oligonucleotide

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<210> 11
 <211> 39
 <212> DNA
 <213> Artificial sequence

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<220>
 <223> Artificial sequence description: 3' c-myc
 oligonucleotide
 <400> 11

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gatctcaggt cctcctcgga gatcagcttc tgcctcatg

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<210> 12
 <211> 45
 <212> DNA
 <213> Artificial sequence

25

<220>
 <223> Artificial sequence description: 5' MCS
 oligonucleotide

30

<400> 12
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<210> 13
 35 <211> 37

<212> DNA
 <213> Artificial sequence

<220>

5 <223> Artificial sequence description: 3' MCS
 oligonucleotide

<400> 13
 cgcggccgca cccgggaatt gcatgcaggt cgaccga

37

10 <210> 14
 <211> 22
 <212> DNA
 <213> Artificial sequence

15 <220>
 <223> Artificial sequence description: 3' mMBP1
 oligonucleotide

<400> 14
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 <210> 15
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 <221> CDS
 <222> (49)..(1377)

30 <220>
 <223> Artificial sequence description: murine MBP1
 (complete sequence)

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Phe Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala Phe Leu Leu	
5 10 15	
ttg ctc ttg gga gca gcg tcc cca cag gat ccc gag gag ccg gac agc	153
Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu Pro Asp Ser	
20 25 30 35	
tac acg gaa tgc aca gat ggc tat gag tgg gat gca gac agc cag cac	201
Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp Ser Gln His	
40 45 50	
tgc cgg gat gtc aac gag tgc ctg acc atc ccg gag gct tgc aag ggt	249
Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala Cys Lys Gly	
55 60 65	
gag atg aaa tgc atc aac cac tac ggg ggt tat ttg tgt ctg cct cgc	297
Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys Leu Pro Arg	
70 75 80	
tct gct gcc gtc atc agt gat ctc cat ggt gaa gga cct cca ccg cca	345
Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro Pro Pro Pro	
85 90 95	
gcg gcc cat gct caa caa cca aac cct tgc ccg cag ggc tac gag cct	393
Ala Ala His Ala Gln Gln Pro Asn Pro Cys Pro Gln Gly Tyr Glu Pro	
100 105 110 115	
gat gaa cag gag agc tgt gtg gat gtg gac gag tgt acc cag gct ttg	441
Asp Glu Gln Glu Ser Cys Val Asp Val Asp Glu Cys Thr Gln Ala Leu	
120 125 130	
cat gac tgt cgc cct agt cag gac tgc cat aac ctt cct ggc tcc tac	489
His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro Gly Ser Tyr	
135 140 145	
cag tgc acc tgc cct gat ggt tac cga aaa att gga ccc gaa tgt gtg	537
Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val	
150 155 160	
gac ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac	585
Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn	
165 170 175	
ctg ccg ggc tct ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga	633
Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly	
180 185 190 195	
cct aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc	681
Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala	
200 205 210	
cca tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc	729
Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg	
215 220 225	
tgt aac cag ggc tat gag ctg cac cgg gat ggc ttc tcc tgc agc gat	777
Cys Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp	

230	235	240	
atc gat gag tgc ggc tac tcc agt tac ctc tgc cag tac cgc tgt gtc			825
Ile Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val			
245	250	255	
aac gag cca ggc cga ttc tcc tgt cac tgc cca caa ggc tac cag ctg			873
Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu			
260	265	270	275
ctg gct aca agg ctc tgc caa gat att gac gag tgt gaa aca ggt gca			921
Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala			
	280	285	290
cac caa tgt tct gag gcc caa acc tgt gtc aac ttc cat ggg ggt tac			969
His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr			
	295	300	305
cgc tgt gtg gac acc aac cgt tgt gtg gag ccc tat gtc caa gtg tca			1017
Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser			
	310	315	320
gac aac cgc tgc ctc tgc cct gcc tcc aat ccc ctt tgt cga gag cag			1065
Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln			
	325	330	335
cct tca tcc att gtg cac cgc tac atg agc atc acc tca gag cga agt			1113
Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser			
	340	345	350
gtg cct gct gac gtg ttt cag atc cag gca acc tct gtc tac cct ggt			1161
Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly			
	360	365	370
gcc tac aat gcc ttt cag atc cgt tct gga aac aca cag ggg gac ttc			1209
Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe			
	375	380	385
tac att agg caa atc aac aat gtc agc gcc atg ctg gtc ctc gcc agg			1257
Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg			
	390	395	400
cca gtg acg gga ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc			1305
Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr			
	405	410	415
atg aat tcc ctt atg agc tac cgg gcc agc tct gta ctg aga ctc acg			1353
Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr			
	420	425	430
gtc ttt gtg gga gcc tat acc ttc tgaagacct cagggaaggg ccatgtgggg			1407
Val Phe Val Gly Ala Tyr Thr Phe			
	440		
gccccctccc cctcccatag ctttaagcagc cccgggggcc tagggatgac cgttctgctt			1467
aaaggaacta tgatgtgaag gacaataaag ggagaaagaa ggaaaa			1513

	<210>	16
	<211>	443
	<212>	PRT
	<213>	Artificial sequence
5	<223>	Artificial sequence description: murine MBP1 (complete sequence)

<400> 16

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 Phe Leu Leu Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu
 20 25 30
 Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp
 35 40 45
 Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala
 50 55 60
 Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys
 65 70 75 80
 Leu Pro Arg Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro
 85 90 95
 Pro Pro Pro Ala Ala His Ala Gln Gln Pro Asn Pro Cys Pro Gln Gly
 100 105 110
 Tyr Glu Pro Asp Glu Gln Glu Ser Cys Val Asp Val Asp Glu Cys Thr
 115 120 125
 Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro
 130 135 140
 Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro
 145 150 155 160
 Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg
 165 170 175
 Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe
 180 185 190
 Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp
 195 200 205
 Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe
 210 215 220
 Leu Cys Arg Cys Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser
 225 230 235 240
 Cys Ser Asp Ile Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr
 245 250 255
 Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly
 260 265 270

Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu
 275 280 285
 Thr Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His
 290 295 300
 Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val
 305 310 315 320
 Gln Val Ser Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys
 325 330 335
 Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser
 340 345 350
 Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val
 355 360 365
 Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln
 370 375 380
 Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val
 385 390 395 400
 Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu
 405 410 415
 Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu
 420 425 430
 Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe
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<210> 17
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 5 <212> DNA
 <213> Artificial sequence

<220>
 <223> Artificial sequence description: 3' hMBP1
 10 oligonucleotide

<400> 17
 ctccgctccg aggtgatggt c

21

<210> 18
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 <212> DNA
 <213> Artificial sequence

<220>

<223> Artificial sequence description: 5' hMBP1
oligonucleotide

5

<400> 18

tgtagctact ccagctacct c

21

<210> 19

<211> 1122

10 <212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: human MBP1 cDNA
(partial sequence)

15

<400> 19

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cttgggatca gcttctcttc aggattctga agagcccgac agctacacgg aatgcacaga 180
tggctatgag tgggaccagc acagccagca ctgccgggat gtcaacgagt gtctgaccat 240
ccctgaggcc tgcaaggggg aaatgaagtg catcaaccac tacggggggct acttgtgcct 300
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<210> 20

20 <211> 684

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: human MBP1 cDNA
(partial sequence)

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tgtctctgcc cggcctccaa cctcttatgt cgagagcagc cttcatccat tgtgcaccgc 300
tacatgacca tcacctcgga gaggagcgtg ccgctgacg tgttccagat ccaggcgacc 360
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ttttacatta ggcaaatcaa caacgtcagc gccatgctgg tcctcgcccg gccggtgacg 480
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cgggccagct ctgtactgag gctcaccgtc tttgtagggg cctacacctt ctgaggagca 600
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<210> 21

<211> 1480

<212> DNA

10 <213> Artificial sequence

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<221> CDS

<222> (59)..(1387)

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<220>

<223> Artificial sequence description: human MBP1
(complete sequence)

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Met Leu Pro Cys Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala															
1 5 10 15															
ctg cta ctg ttg ctc ttg gga tca gct tct cct cag gat tct gaa gag	154														
Leu Leu Leu Leu Leu Leu Gly Ser Ala Ser Pro Gln Asp Ser Glu Glu															
20 25 30															
ccc gac agc tac acg gaa tgc aca gat ggc tat gag tgg gac cca gac	202														
Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Pro Asp															
35 40 45															
agc cag cac tgc cgg gat gtc aac gag tgt ctg acc atc cct gag gcc	250														
Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala															
50 55 60															
tgc aag ggg gaa atg aag tgc atc aac cac tac ggg ggc tac ttg tgc	298														
Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys															
65 70 75 80															
ctg ccc cgc tcc gct gcc gtc atc aac gac cta cac ggc gag gga ccc	346														
Leu Pro Arg Ser Ala Ala Val Ile Asn Asp Leu His Gly Glu Gly Pro															
85 90 95															
ccg cca cca gtg cct ccc gct caa cac ccc aac ccc tgc cca cca ggc	394														
Pro Pro Pro Val Pro Pro Ala Gln His Pro Asn Pro Cys Pro Pro Gly															
100 105 110															
tat gag ccc gac gat cag gac agc tgt gtg gat gtg gac gag tgt gcc	442														
Tyr Glu Pro Asp Asp Gln Asp Ser Cys Val Asp Val Asp Glu Cys Ala															
115 120 125															
cag gcc ctg cac gac tgt cgc ccc agc cag gac tgc cat aac ttg cct	490														
Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro															
130 135 140															
ggc tcc tat cag tgc acc tgc cct gat ggt tac cgc aag atc ggg ccc	538														
Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro															
145 150 155 160															
gag tgt gtg gac ata gac gag tgc cgc tac cgc tac tgc cag cac cgc	586														
Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg															
165 170 175															
tgc gtg aac ctg cct ggc tcc ttc cgc tgc cag tgc gag ccg ggc ttc	634														

Cys	Val	Asn	Leu	Pro	Gly	Ser	Phe	Arg	Cys	Gln	Cys	Glu	Pro	Gly	Phe			
180																185	190	
cag	ctg	ggg	cct	aac	aac	cgc	tcc	tgt	gtt	gat	gtg	aac	gag	tgt	gac	682		
Gln	Leu	Gly	Pro	Asn	Asn	Arg	Ser	Cys	Val	Asp	Val	Asn	Glu	Cys	Asp			
195																200	205	
atg	ggg	gcc	cca	tgc	gag	cag	cgc	tgc	ttc	aac	tcc	tat	ggg	acc	ttc	730		
Met	Gly	Ala	Pro	Cys	Glu	Gln	Arg	Cys	Phe	Asn	Ser	Tyr	Gly	Thr	Phe			
210																215	220	
ctg	tgt	cgc	tgc	cac	cag	ggc	tac	gag	ctg	cat	cgg	gat	ggc	ttc	tcc	778		
Leu	Cys	Arg	Cys	His	Gln	Gly	Tyr	Glu	Leu	His	Arg	Asp	Gly	Phe	Ser			
225																230	235	240
tgc	agt	gat	att	gat	gag	tgt	agc	tac	tcc	agc	tac	ctc	tgt	cag	tac	826		
Cys	Ser	Asp	Ile	Asp	Glu	Cys	Ser	Tyr	Ser	Ser	Tyr	Leu	Cys	Gln	Tyr			
245																250	255	
cgc	tgc	gtc	aac	gag	cca	ggc	cgt	ttc	tcc	tgc	cac	tgc	cca	cag	ggc	874		
Arg	Cys	Val	Asn	Glu	Pro	Gly	Arg	Phe	Ser	Cys	His	Cys	Pro	Gln	Gly			
260																265	270	
tac	cag	ctg	ctg	gcc	aca	cgc	ctc	tgc	caa	gac	att	gat	gag	tgt	gag	922		
Tyr	Gln	Leu	Leu	Ala	Thr	Arg	Leu	Cys	Gln	Asp	Ile	Asp	Glu	Cys	Glu			
275																280	285	
tct	ggt	gcg	cac	cag	tgc	tcc	gag	gcc	caa	acc	tgt	gtc	aac	ttc	cat	970		
Gly	Ala	His	Gln	Cys	Ser	Glu	Ala	Gln	Thr	Cys	Val	Asn	Phe	His				
290																295	300	
ggg	ggc	tac	cgc	tgc	gtg	gac	acc	aac	cgc	tgc	gtg	gag	ccc	tac	atc	1018		
Gly	Gly	Tyr	Arg	Cys	Val	Asp	Thr	Asn	Arg	Cys	Val	Glu	Pro	Tyr	Ile			
305																310	315	320
cag	gtc	tct	gag	aac	cgc	tgt	ctc	tgc	ccg	gcc	tcc	aac	cct	cta	tgt	1066		
Gln	Val	Ser	Glu	Asn	Arg	Cys	Leu	Cys	Pro	Ala	Ser	Asn	Pro	Leu	Cys			
325																330	335	
cga	gag	cag	cct	tca	tcc	att	gtg	cac	cgc	tac	atg	acc	atc	acc	tcg	1114		
Arg	Glu	Gln	Pro	Ser	Ser	Ile	Val	His	Arg	Tyr	Met	Thr	Ile	Thr	Ser			
340																345	350	
gag	cgg	agc	gtg	ccc	gct	gac	gtg	ttc	cag	atc	cag	gcg	acc	tcc	gtc	1162		
Glu	Arg	Ser	Val	Pro	Ala	Asp	Val	Phe	Gln	Ile	Gln	Ala	Thr	Ser	Val			
355																360	365	
tac	ccc	ggt	gcc	tac	aat	gcc	ttt	cag	atc	cgt	gct	gga	aac	tcg	cag	1210		
Tyr	Pro	Gly	Ala	Tyr	Asn	Ala	Phe	Gln	Ile	Arg	Ala	Gly	Asn	Ser	Gln			
370																375	380	
ggg	gac	ttt	tac	att	agg	caa	atc	aac	aac	gtc	agc	gcc	atg	ctg	gtc	1258		
Gly	Asp	Phe	Tyr	Ile	Arg	Gln	Ile	Asn	Asn	Val	Ser	Ala	Met	Leu	Val			
385																390	395	400
ctc	gcc	cgg	ccg	gtg	acg	ggc	ccc	cgg	gag	tac	gtg	ctg	gac	ctg	gag	1306		
Leu	Ala	Arg	Pro	Val	Thr	Gly	Pro	Arg	Glu	Tyr	Val	Leu	Asp	Leu	Glu			
405																410	415	

atg gtc acc atg aat tcc ctc atg agc tac cgg gcc agc tct gta ctg 1354
 Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu
 420 425 430

agg ctc acc gtc ttt gta ggg gcc tac acc ttc tgaggagcag gagggagcca 1407
 Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe
 435 440

ccctccctgc agctacccta gctgaggagc ctgttctgag gggcagaatg agaaaggcaa 1467
 taaagggaga aag 1480

- 5 <210> 22
 <211> 443
 <212> PRT
 <213> Artificial sequence
 <223> Artificial sequence description: human MBP1
 (complete sequence)

Met Leu Pro Cys Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala
1 5 10 15

Leu Leu Leu Leu Leu Leu Gly Ser Ala Ser Pro Gln Asp Ser Glu Glu
20 25 30

Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Pro Asp
35 40 45

Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala
50 55 60

Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys
65 70 75 80

Leu Pro Arg Ser Ala Ala Val Ile Asn Asp Leu His Gly Glu Gly Pro
85 90 95

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Pro Pro Pro Val Pro Pro Ala Gln His Pro Asn Pro Cys Pro Pro Gly
      100                      105                  110
```

Tyr Glu Pro Asp Asp Gln Asp Ser Cys Val Asp Val Asp Glu Cys Ala
115 120 125

Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro
130 135 140

Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro
145 150 155 160

Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg
165 170 175

Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe
180 185 190

Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp
195 200 205

Met	Gly	Ala	Pro	Cys	Glu	Gln	Arg	Cys	Phe	Asn	Ser	Tyr	Gly	Thr	Phe	210	215	220	
Leu	Cys	Arg	Cys	His	Gln	Gly	Tyr	Glu	Leu	His	Arg	Asp	Gly	Phe	Ser	225	230	235	240
Cys	Ser	Asp	Ile	Asp	Glu	Cys	Ser	Tyr	Ser	Ser	Tyr	Leu	Cys	Gln	Tyr	245	250	255	
Arg	Cys	Val	Asn	Glu	Pro	Gly	Arg	Phe	Ser	Cys	His	Cys	Pro	Gln	Gly	260	265	270	
Tyr	Gln	Leu	Leu	Ala	Thr	Arg	Leu	Cys	Gln	Asp	Ile	Asp	Glu	Cys	Glu	275	280	285	
Ser	Gly	Ala	His	Gln	Cys	Ser	Glu	Ala	Gln	Thr	Cys	Val	Asn	Phe	His	290	295	300	
Gly	Gly	Tyr	Arg	Cys	Val	Asp	Thr	Asn	Arg	Cys	Val	Glu	Pro	Tyr	Ile	305	310	315	320
Gln	Val	Ser	Glu	Asn	Arg	Cys	Leu	Cys	Pro	Ala	Ser	Asn	Pro	Leu	Cys	325	330	335	
Arg	Glu	Gln	Pro	Ser	Ser	Ile	Val	His	Arg	Tyr	Met	Thr	Ile	Thr	Ser	340	345	350	
Glu	Arg	Ser	Val	Pro	Ala	Asp	Val	Phe	Gln	Ile	Gln	Ala	Thr	Ser	Val	355	360	365	
Tyr	Pro	Gly	Ala	Tyr	Asn	Ala	Phe	Gln	Ile	Arg	Ala	Gly	Asn	Ser	Gln	370	375	380	
Gly	Asp	Phe	Tyr	Ile	Arg	Gln	Ile	Asn	Asn	Val	Ser	Ala	Met	Leu	Val	385	390	395	400
Leu	Ala	Arg	Pro	Val	Thr	Gly	Pro	Arg	Glu	Tyr	Val	Leu	Asp	Leu	Glu	405	410	415	
Met	Val	Thr	Met	Asn	Ser	Leu	Met	Ser	Tyr	Arg	Ala	Ser	Ser	Val	Leu	420	425	430	
Arg	Leu	Thr	Val	Phe	Val	Gly	Ala	Tyr	Thr	Phe						435	440		

<210> 23

5 <211> 817

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: murine MBP1
cDNA (partial sequence)

<400> 23

gctgtggcag aaacccctga cttctgcca ccacctcca gctcaggat gctccctttt 60
gcttcctgcc tccccgggtc tttgctgctc tgggcgtttc tgctgttgct cttgggagca 120
gcgtccccac aggatcccgga ggagccggac agctacacgg aatgcacaga tggctatgag 180
tgggatgcag acagccagca ctgccgggat gtcaacgagt gcctgaccat cccggaggct 240
tgcaagggtg agatgaaatg catcaaccac tacgggggtt atttgtgtct gcctcgtctc 300
gctgccgtca tcagtgatct ccatggtgaa ggacctccac cgccagcggc ccatgctcaa 360
caaccaaacc cttgcccgca gggctacgag cctgatgaac aggagagctg tgtggatgtg 420
gacgagtgtg cccaggcttt gcatgactgt cgccctagtc aggactgcca taaccttctc 480
ggctcctacc agtgcacctg cctgatggtt taccgaaaaa ttggaccgca atgtgtggac 540
atagatgagt gtcgttaccg ctattgccag catcgatgtg tgaacctgcc gggctctttt 600
cgatgccagt gtgagccagg cttccagttg ggacctaaaca accgctcttg tgtggatgtg 660
aatgagtgtg acatgggagc cccatgtgag cagcgctgct tcaactccta tgggaccttc 720
ctgtgtcgct gtaaccaggg ctatgagctg caccgggagc gcttctcctg cagcgatata 780
gatgagtgcg gctactccag ttacctctgc cagtacc 817

5

<210> 24

<211> 24

<212> DNA

<213> Artificial sequence

10

<220>

<223> Artificial sequence description: sense-GAPDH
oligonucleotide

<400> 24

cggagtcaac ggatttgggc gtat

24

15

<210> 25

<211> 24

<212> DNA

20

<213> Artificial sequence

<220>

<223> Artificial sequence description: antisense-GAPDH
oligonucleotide

25

<400> 25

agccttctcc atggtgggtga agac

24

<210> 26
 <211> 25
 <212> DNA
 <213> Artificial sequence

5

<220>
 <223> Artificial sequence description: oligonucleotide

<400> 26
 cggttgacct tggggttcag ggggg

25

10

<210> 27
 <211> 21
 <212> DNA
 <213> Artificial sequence

15

<220>
 <223> Artificial sequence description: sense MBP1
 oligonucleotide

<400> 27
 gccctgatgg ttaccgcaag a

21

20

<210> 28
 <211> 21
 <212> DNA
 <213> Artificial sequence

25

<220>
 <223> Artificial sequence description: antisense MBP1
 oligonucleotide

30

<400> 28
 agcccccatg gaagtgaca c

21

<210> 29
 <211> 20

<212> DNA

<213> Artificial sequence

<220>

5 <223> Artificial sequence description: sense-actin
oligonucleotide

<400> 29

gtggggcgcc ccaggcacca

20

10 <210> 30

<211> 1358

<212> DNA

<213> Artificial sequence

15 <220>

<221> CDS

<222> (1)..(885)

<220>

20 <223> Artificial sequence description: human MBP1
C-term fragment

<400> 30

tgc acc tgc cct gat ggt tac cgc aag atc ggg ccc gag tgt gtg gac 48
Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp
1 5 10 15

ata gac gag tgc cgc tac cgc tac tgc cag cac cgc tgc gtg aac ctg 96
Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu
20 25 30

cct ggc tcc ttc cgc tgc cag tgc gag ccg ggc ttc cag ctg ggg cct 144
Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
35 40 45

aac	aac	cgc	tcc	tgt	gtt	gat	gtg	aac	gag	tgt	gac	atg	ggg	gcc	cca	192
Asn	Asn	Arg	Ser	Cys	Val	Asp	Val	Asn	Glu	Cys	Asp	Met	Gly	Ala	Pro	
50						55					60					
tgc	gag	cag	cgc	tgc	tcc	aac	tcc	tat	ggg	acc	tcc	ctg	tgt	cgc	tgc	240
Cys	Glu	Gln	Arg	Cys	Phe	Asn	Ser	Tyr	Gly	Thr	Phe	Leu	Cys	Arg	Cys	
65				70					75						80	
cac	cag	ggc	tat	gag	ctg	cat	cgg	gat	ggc	tcc	tcc	tgc	agt	gat	att	288
His	Gln	Gly	Tyr	Glu	Leu	His	Arg	Asp	Gly	Phe	Ser	Cys	Ser	Asp	Ile	
				85					90					95		
gat	gag	tgt	agc	tac	tcc	agc	tac	ctc	tgt	cag	tac	cgc	tgc	gtc	aac	336
Asp	Glu	Cys	Ser	Tyr	Ser	Ser	Tyr	Leu	Cys	Gln	Tyr	Arg	Cys	Val	Asn	
			100					105					110			
gag	cca	ggc	cgt	tcc	tcc	tgc	cac	tgc	cca	cag	ggt	tac	cag	ctg	ctg	384
Glu	Pro	Gly	Arg	Phe	Ser	Cys	His	Cys	Pro	Gln	Gly	Tyr	Gln	Leu	Leu	
		115					120					125				
gcc	aca	cgc	ctc	tgc	caa	gac	att	gat	gag	tgt	gag	tct	ggg	gcg	cac	432
Ala	Thr	Arg	Leu	Cys	Gln	Asp	Ile	Asp	Glu	Cys	Glu	Ser	Gly	Ala	His	
	130					135					140					
cag	tgc	tcc	gag	gcc	caa	acc	tgt	gtc	aac	tcc	cat	ggg	ggc	tac	cgc	480
Gln	Cys	Ser	Glu	Ala	Gln	Thr	Cys	Val	Asn	Phe	His	Gly	Gly	Tyr	Arg	
145				150						155					160	
tgc	gtg	gac	acc	aac	cgc	tgc	gtg	gag	ccc	tac	atc	cag	gtc	tct	gag	528
Cys	Val	Asp	Thr	Asn	Arg	Cys	Val	Glu	Pro	Tyr	Ile	Gln	Val	Ser	Glu	
				165				170						175		
aac	cgc	tgt	ctc	tgc	ccg	gcc	tcc	aac	cct	cta	tgt	cga	gag	cag	cct	576
Asn	Arg	Cys	Leu	Cys	Pro	Ala	Ser	Asn	Pro	Leu	Cys	Arg	Glu	Gln	Pro	
			180					185					190			
tca	tcc	att	gtg	cac	cgc	tac	atg	acc	atc	acc	tcg	gag	cgg	agc	gtg	624
Ser	Ser	Ile	Val	His	Arg	Tyr	Met	Thr	Ile	Thr	Ser	Glu	Arg	Ser	Val	
		195					200					205				
ccc	gct	gac	gtg	tcc	cag	atc	cag	gcg	acc	tcc	gtc	tac	ccc	ggg	gcc	672
Pro	Ala	Asp	Val	Phe	Gln	Ile	Gln	Ala	Thr	Ser	Val	Tyr	Pro	Gly	Ala	
	210					215					220					
tac	aat	gcc	ttt	cag	atc	cgt	gct	gga	aac	tcg	cag	ggg	gac	ttt	tac	720
Tyr	Asn	Ala	Phe	Gln	Ile	Arg	Ala	Gly	Asn	Ser	Gln	Gly	Asp	Phe	Tyr	
225				230						235					240	
att	agg	caa	atc	aac	aac	gtc	agc	gcc	atg	ctg	gtc	ctc	gcc	cgg	cgg	768
Ile	Arg	Gln	Ile	Asn	Asn	Val	Ser	Ala	Met	Leu	Val	Leu	Ala	Arg	Pro	
				245				250								

275

280

285

ttt gta ggg gcc tac acc ttc tgaggagcag gagggagcca cctccctgc 915
 Phe Val Gly Ala Tyr Thr Phe
 290 295

agctacccta gctgaggagc ctgttgtag gggcagaatg agaaaggcaa taaagggaga 975
 aagaaagtcc tggtaggctga ggtgggcggg tcacactgca ggaagcctca ggctggggca 1035
 gggtaggcact tggggggggca ggccaagtgc acctaaatgg ggggtctctat atgttcaggc 1095
 ccagggggccc ccattgacag gagctgggag ctctgcacca cgagcttcag tcaccccgag 1155
 aggagaggag gtaacgagga gggcgggactc caggccccgg ccagagagatt tggacttggc 1215
 tggcttgtag gggtcctaag aaactccact ctggacagcg ccaggaggcc ctgggttcca 1275
 ttcctaactc tgcctcaaac tgtacatttg gataagccct agtagttccc tgggcctgtt 1335
 tttctataaa acgaggcaac tgg 1358

- <210> 31
 <211> 295
 5 <212> PRT
 <213> Artificial sequence
 <223> Artificial sequence description: human MBP1
 C-term fragment

Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp
1 5 10 15

Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
35 40 45

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys
65 70 75 80

Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn
100 105 110

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Ser Gly Ala His
130 135 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg

145		150		155		160
Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile Gln Val Ser Glu						
		165		170		175
Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro						
		180		185		190
Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser Glu Arg Ser Val						
		195		200		205
Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala						
		210		215		220
Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln Gly Asp Phe Tyr						
		225		230		235
Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro						
		245		250		255
Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met						
		260		265		270
Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val						
		275		280		285
Phe Val Gly Ala Tyr Thr Phe						
		290		295		

<210> 32
 <211> 1663
 <212> DNA

5 <213> Artificial sequence

<220>
 <221> CDS
 <222> (1)..(999)

10

<220>
 <223> Artificial sequence description: murine fibulin
 2 c-term fragment

<400> 32															
gag ggc tct gaa tgt gtg gat gtg aat gag tgt gag aca ggt gtg cat	48														
Glu Gly Ser Glu Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val His															
1 5 10 15															
cgc tgt ggc gag ggc caa ctg tgc tat aac ctc cct gga tcc tac cgc															96
Arg Cys Gly Glu Gly Gln Leu Cys Tyr Asn Leu Pro Gly Ser Tyr Arg															
20 25 30															
tgt gac tgc aag ccc ggc ttc cag agg gat gca ttc ggc agg act tgc															144
Cys Asp Cys Lys Pro Gly Phe Gln Arg Asp Ala Phe Gly Arg Thr Cys															
35 40 45															
att gat gtg aac gaa tgc tgg gtc tcg ccg ggc cgc ctg tgc cag cac															192
Ile Asp Val Asn Glu Cys Trp Val Ser Pro Gly Arg Leu Cys Gln His															

50	55	60	
aca tgt gag aac aca ccg ggc tcc tac cgc tgc tcc tgc gct gct ggc Thr Cys Glu Asn Thr Pro Gly Ser Tyr Arg Cys Ser Cys Ala Ala Gly 65 70 75 80			240
ttc ctt ttg gcc gca gat ggc aaa cat tgt gaa gat gtg aac gag tgc Phe Leu Leu Ala Ala Asp Gly Lys His Cys Glu Asp Val Asn Glu Cys 85 90 95			288
gag act cgg cgc tgc agc cag gaa tgt gcc aac atc tat ggc tcc tat Glu Thr Arg Arg Cys Ser Gln Glu Cys Ala Asn Ile Tyr Gly Ser Tyr 100 105 110			336
cag tgc tac tgc cgt cag ggc tac cag ctg gca gag gat ggg cat acc Gln Cys Tyr Cys Arg Gln Gly Tyr Gln Leu Ala Glu Asp Gly His Thr 115 120 125			384
tgc aca gac atc gat gag tgt gca cag ggc gcg ggc att ctc tgt acc Cys Thr Asp Ile Asp Glu Cys Ala Gln Gly Ala Gly Ile Leu Cys Thr 130 135 140			432
ttc cgc tgt gtc aac gtg cct ggg agc tac cag tgt gca tgc cca gag Phe Arg Cys Val Asn Val Pro Gly Ser Tyr Gln Cys Ala Cys Pro Glu 145 150 155 160			480
caa ggg tat aca atg atg gcc aac ggg agg tcc tgc aag gac ctg gat Gln Gly Tyr Thr Met Met Ala Asn Gly Arg Ser Cys Lys Asp Leu Asp 165 170 175			528
gag tgt gca ctg ggc acc cac aac tgc tct gag gct gag acc tgc cac Glu Cys Ala Leu Gly Thr His Asn Cys Ser Glu Ala Glu Thr Cys His 180 185 190			576
aat atc cag ggg agt ttc cgc tgc ctg cgc ttt gat tgt cca ccc aac Asn Ile Gln Gly Ser Phe Arg Cys Leu Arg Phe Asp Cys Pro Pro Asn 195 200 205			624
tat gtc cgt gtc tca caa acg aag tgc gag cgc acc aca tgc cag gat Tyr Val Arg Val Ser Gln Thr Lys Cys Glu Arg Thr Thr Cys Gln Asp 210 215 220			672
atc acg gaa tgt caa acc tca cca gct cgc atc acg cac tac cag ctc Ile Thr Glu Cys Gln Thr Ser Pro Ala Arg Ile Thr His Tyr Gln Leu 225 230 235 240			720
aat ttc cag aca ggc cta ctg gta cct gca cat atc ttc cgc atc ggc Asn Phe Gln Thr Gly Leu Leu Val Pro Ala His Ile Phe Arg Ile Gly 245 250 255			768
cct gct ccc gcc ttt gct ggg gac acc atc tcc ctg acc atc acg aag Pro Ala Pro Ala Phe Ala Gly Asp Thr Ile Ser Leu Thr Ile Thr Lys 260 265 270			816
ggc aat gag gag ggc tac ttc gtc aca cgc aga ctc aat gcc tac act Gly Asn Glu Glu Gly Tyr Phe Val Thr Arg Arg Leu Asn Ala Tyr Thr 275 280 285			864
ggg gtg gta tcc ctg cag cgg tct gtc ctg gag ccg cgg gac ttt gcc			912

Gly Val Val Ser Leu Gln Arg Ser Val Leu Glu Pro Arg Asp Phe Ala
 290 295 300

cta gat gtg gag atg aag ctt tgg cgc cag ggc tct gtc act acc ttc 960
 Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe
 305 310 315 320

ctg gcc aag atg tac acc ttc ttc acc act ttt gcc cca tgaggtgaca 1009
 Leu Ala Lys Met Tyr Ile Phe Phe Thr Thr Phe Ala Pro
 325 330

tgtcaggcaa tccctccagg tgatgcctgg gcggtgggca gctgcgccac tccaaagtgg 1069
 ctttttgcgtg tgactctgta acttaactta atcatgctga gctggttggc cttgagcttc 1129
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 caaggaaaaa tgaaagaaat cattttaaaa gggttttttt tttgctgttg ttgtttaatg 1609
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<210> 33

<211> 333

5 <212> PRT

<213> Artificial sequence

<223> Artificial sequence description: murine fibulin
 2 c-term fragment

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Phe Leu Leu Ala Ala Asp Gly Lys His Cys Glu Asp Val Asn Glu Cys
85 90 95

$\{f^{(1)}_1, f^{(1)}_2, \dots, f^{(1)}_n\}$ and $\{f^{(2)}_1, f^{(2)}_2, \dots, f^{(2)}_n\}$ are two sets of functions defined on the interval $[a, b]$. The functions $f^{(1)}_i$ and $f^{(2)}_i$ are assumed to be linearly independent. The functions $f^{(1)}_i$ and $f^{(2)}_i$ are assumed to be linearly independent. The functions $f^{(1)}_i$ and $f^{(2)}_i$ are assumed to be linearly independent.

Glu Thr Arg Arg Cys Ser Gln Glu Cys Ala Asn Ile Tyr Gly Ser Tyr
 100 105 110

Gln Cys Tyr Cys Arg Gln Gly Tyr Gln Leu Ala Glu Asp Gly His Thr
 115 120 125

Cys Thr Asp Ile Asp Glu Cys Ala Gln Gly Ala Gly Ile Leu Cys Thr
 130 135 140

Phe Arg Cys Val Asn Val Pro Gly Ser Tyr Gln Cys Ala Cys Pro Glu
 145 150 155 160

Gln Gly Tyr Thr Met Met Ala Asn Gly Arg Ser Cys Lys Asp Leu Asp
 165 170 175

Glu Cys Ala Leu Gly Thr His Asn Cys Ser Glu Ala Glu Thr Cys His
 180 185 190

Asn Ile Gln Gly Ser Phe Arg Cys Leu Arg Phe Asp Cys Pro Pro Asn
 195 200 205

Tyr Val Arg Val Ser Gln Thr Lys Cys Glu Arg Thr Thr Cys Gln Asp
 210 215 220

Ile Thr Glu Cys Gln Thr Ser Pro Ala Arg Ile Thr His Tyr Gln Leu
 225 230 235 240

Asn Phe Gln Thr Gly Leu Leu Val Pro Ala His Ile Phe Arg Ile Gly
 245 250 255

Pro Ala Pro Ala Phe Ala Gly Asp Thr Ile Ser Leu Thr Ile Thr Lys
 260 265 270

Gly Asn Glu Glu Gly Tyr Phe Val Thr Arg Arg Leu Asn Ala Tyr Thr
 275 280 285

Gly Val Val Ser Leu Gln Arg Ser Val Leu Glu Pro Arg Asp Phe Ala
 290 295 300

Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe
 305 310 315 320

Leu Ala Lys Met Tyr Ile Phe Phe Thr Thr Phe Ala Pro
 325 330